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RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/10/042,894A

TIME: 09:54:24

Input Set : A:\1286 AMD SEQLIST.TXT

Output Set: N:\CRF3\06052002\J042894A.raw

P6
ENTERED

4 <110> APPLICANT: Shi, Jinrui
 5 Beach, Larry
 6 Wang, Hongyu
 7 Rafalski, Antoni J.
 8 Cahoon, Rebecca E.
 10 <120> TITLE OF INVENTION: Novel Inositol Polyphosphate Kinase
 11 Genes and Uses Thereof
 13 <130> FILE REFERENCE: 1286
 15 <140> CURRENT APPLICATION NUMBER: US 10/042,894A
 16 <141> CURRENT FILING DATE: 2002-01-09
 18 <150> PRIOR APPLICATION NUMBER: US 60/261,465
 19 <151> PRIOR FILING DATE: 2001-01-12
 21 <160> NUMBER OF SEQ ID NOS: 37
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1169
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Zea mays
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 31 <221> NAME/KEY: CDS
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 36 cttgtctcca tagtcccat acc atg ccc gac ctc cac ccg ccg gag cac caa 113
 37 Met Pro Asp Leu His Pro Pro Glu His Gln
 38 1 5 10
 40 gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc ccg ctc atc gac 161
 41 Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
 42 15 20 25
 44 ggc tcc ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag 209
 45 Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
 46 30 35 40
 48 cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg 257
 49 His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro
 50 45 50 55
 52 gcc cgc atc cga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc 305
 53 Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
 54 60 65 70
 56 ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc 353
 57 Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
 58 75 80 85 90
 60 gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag 401
 61 Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys

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62          95          100          105
64 atc ggc gcc atc acg tgg cca ccg agt tcg ccg gag ccc tac atc gcc 449
65 Ile Gly Ala Ile Thr Trp Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala
66          110          115          120
68 aag tac ctc gcc aag gac cgc ggg acc acg agc gtt ctg ctc gga ttc 497
69 Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe
70          125          130          135
72 cgc gtc ttg cgt ccg agt cgt cgg ccc cga ggg cgc cgt gtg gcg gac 545
73 Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Arg Val Ala Asp
74          140          145          150
76 gga gcg ccc gga ggt gaa ggc tat gga cac cgt cgg cgt ccg ccg cgt 593
77 Gly Ala Pro Gly Gly Glu Gly Tyr Gly His Arg Arg Arg Pro Pro Arg
78 155          160          165          170
80 gct ccg gcg cta cgt gtc atc cgc ttg ccg acg agg gga tgg act gcg 641
81 Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala
82          175          180          185
84 cgc tcg cgg cgg cgg tgt acg gag gaa aag gtg gag tct tgt cac agc 689
85 Arg Ser Arg Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser
86          190          195          200
88 tgc gcg agc tca agg cat ggt tgg agg agc aga ctc tgt tcc act tct 737
89 Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser
90          205          210          215
92 act cgg cgt cga ttc ttc tgg gct atg atg ctg ctg cag tcg cag cag 785
93 Thr Arg Arg Arg Phe Phe Trp Ala Met Met Leu Leu Gln Ser Gln Gln
94          220          225          230
96 gcg gag gtg ggg gtg ggg taa cagtgaagct ggtggacttt gcccatgtgg 836
97 Ala Glu Val Gly Val Gly *
98 235          240
100 ccgaggggtga tgggggtgatt gaccacaact tcttgggcga gctctgctag ctgatcaagt 896
101 tcgttttctga cattgttcca gagactcctt agacgcagcc tttgggtcct tcttaagaga 956
102 ggatcctgac atttttgatt tgataacaaa ggaagcactt tcagctgcaa aaaaagaaag 1016
103 cagcagtga gatgaagatg acagtagtga ggaaagttcg gatgatgagc caacaaaagt 1076
104 tgaagaaaag aaggctccaa aagtatcaga aaacattgga tctgaggatg aatcttctga 1136
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108 <211> LENGTH: 240
109 <212> TYPE: PRT
110 <213> ORGANISM: Zea mays
112 <400> SEQUENCE: 2
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114 1 5 10 15
115 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
116 20 25 30
117 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
118 35 40 45
119 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr
120 50 55 60
121 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
122 65 70 75 80

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123 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
124                               85                      90                      95
125 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
126                               100                     105                     110
127 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp
128                               115                     120                     125
129 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser
130                               130                     135                     140
131 Arg Arg Pro Arg Gly Arg Arg Val Ala Asp Gly Ala Pro Gly Gly Glu
132 145                               150                     155                     160
133 Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val
134                               165                     170                     175
135 Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys
136                               180                     185                     190
137 Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His
138                               195                     200                     205
139 Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe
140                               210                     215                     220
141 Trp Ala Met Met Leu Leu Gln Ser Gln Gln Ala Glu Val Gly Val Gly
142 225                               230                     235                     240
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 923
147 <212> TYPE: DNA
148 <213> ORGANISM: Zea mays
150 <220> FEATURE:
151 <221> NAME/KEY: CDS
152 <222> LOCATION: (53)...(736)
154 <400> SEQUENCE: 3
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156                               Met Pro
157                               1
159 gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc 106
160 Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
161                               5                      10                      15
163 agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 154
164 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
165                               20                      25                      30
167 ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202
168 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
169 35                               40                      45                      50
171 ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 250
172 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
173                               55                      60                      65
175 ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298
176 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
177                               70                      75                      80
179 gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346
180 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
181                               85                      90                      95

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183 gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 394
184 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
185 100 105 110
187 agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg 442
188 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly
189 115 120 125 130
191 acc acg agc gtt ctg ctc gga ttc cgc gtc tcc gcc gtc cga gtc gtc 490
192 Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val
193 135 140 145
195 gtc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gct 538
196 Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala
197 150 155 160
199 atg gac acc gtc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc 586
200 Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser
201 165 170 175
203 gct tgc cga cga ggg gat gga ctg cgc gct cgc gcc gcc ggt gta cgg 634
204 Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly Val Arg
205 180 185 190
207 agg aaa agg tgg agt ctt gtc act gct gcg cga gct caa gcc gtg gtt 682
208 Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly Val Val
209 195 200 205 210
211 cga gga gca gcc tct gtt cca ctt cta ctc gcc gtc gat tct tct ggg 730
212 Arg Gly Ala Ala Ser Val Pro Leu Leu Gly Val Asp Ser Ser Gly
213 215 220 225
215 cta tga tgctgctgca gtcgcagcag gcggagggtgg ggggtggggta acagtgaagc 786
216 Leu *
219 tgggtggactt tgcccatgtg gccgaggggtg atgggggtgat tgaccacaac ttctctgggagc 846
220 ggctctgcta gctgatcaag ttcgtttctg acattgttcc agagactcct cagacgcagc 906
221 ctttgggtcc ttcttaa 923
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 227
225 <212> TYPE: PRT
226 <213> ORGANISM: Zea mays
228 <400> SEQUENCE: 4
229 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
230 1 5 10 15
231 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
232 20 25 30
233 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
234 35 40 45
235 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
236 50 55 60
237 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
238 65 70 75 80
239 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
240 85 90 95
241 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
242 100 105 110
243 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp

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244          115          120          125
245 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
246          130          135          140
247 Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
248 145          150          155          160
249 Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val
250          165          170          175
251 Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly
252          180          185          190
253 Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly
254          195          200          205
255 Val Val Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser
256          210          215          220
257 Ser Gly Leu
258 225
261 <210> SEQ ID NO: 5
262 <211> LENGTH: 923
263 <212> TYPE: DNA
264 <213> ORGANISM: Zea mays
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (53)...(922)
270 <400> SEQUENCE: 5
271 accgcttcca ccacgcacac tcgtcaccac ttgctcccat agtcccccata cc atg ccc 58
272                                     Met Pro
273                                     1
275 gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc 106
276 Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
277          5          10          15
279 agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 154
280 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
281          20          25          30
283 ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202
284 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
285 35          40          45          50
287 ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 250
288 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
289          55          60          65
291 ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298
292 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
293          70          75          80
295 gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346
296 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
297          85          90          95
299 gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 394
300 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
301          100          105          110
303 agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg 442
304 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/042,894A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 12,283,481,491,598,617,619,626,637
Seq#:18; N Pos. 9,15,47,135,230,335,359,403,415,419,450,480,507,509,518
Seq#:19; N Pos. 85,226,277,294,317,331,351
Seq#:30; Xaa Pos. 3,12,14,15,18,25,27
Seq#:31; Xaa Pos. 3,12,14,15,18,25,27
Seq#:32; Xaa Pos. 3,12,14,15,18,25,27
Seq#:33; Xaa Pos. 3,12,14,15,18,25,27
Seq#:34; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:35; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:36; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38
Seq#:37; Xaa Pos. 3,6,7,8,9,10,11,19,25,26,27,28,29,31,34,38